```
         10                  30                  50
CAGGGGACATGAGAGGCACACCGAAGACCCACCTCCTGGCCTTCTCCCTCCTCTGCCTCC
       MetArgGlyThrProLysThrHisLeuLeuAlaPheSerLeuLeuCysLeuL
         70                  90                 110
TCTCAAAGGTGCGTACCCAGCTGTGCCCGACACCATGTACCTGCCCCTGGCCACCTCCCC
euSerLysValArgThrGlnLeuCysProThrProCysThrCysProTrpProProProA
        130                 150                 170
GATGCCCGCTGGGAGTACCCCTGGTGCTGGATGGCTGTGGCTGCTGCCGGGTATGTGCAC
rgCysProLeuGlyValProLeuValLeuAspGlyCysGlyCysCysArgValCysAlaA
        190                 210                 230
GGCGGCTGGGGGAGCCCTGCGACCAACTCCACGTCTGCGACGCCAGCCAGGGCCTGGTCT
rgArgLeuGlyGluProCysAspGlnLeuHisValCysAspAlaSerGlnGlyLeuValC
        250                 270                 290
GCCAGCCCGGGGCAGGACCCGGTGGCCGGGGGGCCCTGTGCCTCTTGGCAGAGGACGACA
ysGlnProGlyAlaGlyProGlyGlyArgGlyAlaLeuCysLeuLeuAlaGluAspAspS
        310                 330                 350
GCAGCTGTGAGGTGAACGGCCGCCTGTATCGGGAAGGGGAGACCTTCCAGCCCCACTGCA
erSerCysGluValAsnGlyArgLeuTyrArgGluGlyGluThrPheGlnProHisCysS
        370                 390                 410
GCATCCGCTGCCGCTGCGAGGACGGCGGCTTCACCTGCGTGCCGCTGTGCAGCGAGGATG
erIleArgCysArgCysGluAspGlyGlyPheThrCysValProLeuCysSerGluAspV
        430                 450                 470
TGCGGCTGCCCAGCTGGGACTGCCCCCACCCCAGGAGGGTCGAGGTCCTGGGCAAGTGCT
alArgLeuProSerTrpAspCysProHisProArgArgValGluValLeuGlyLysCysC
        490                 510                 530
GCCCTGAGTGGGTGTGCGGCCAAGGAGGGGGACTGGGGACCCAGCCCCTTCCAGCCCAAG
ysProGluTrpValCysGlyGlnGlyGlyGlyLeuGlyThrGlnProLeuProAlaGlnG
        550                 570                 590
GACCCCAGTTTTCTGGCCTTGTCTCTTCCCTGCCCCCTGGTGTCCCCTGCCCAGAATGGA
lyProGlnPheSerGlyLeuValSerSerLeuProProGlyValProCysProGluTrpS
```

FIG.1A

```
        610                 630                 650
GCACGGCCTGGGGACCCTGCTCGACCACCTGTGGGCTGGGCATGGCCACCCGGGTGTCCA
erThrAlaTrpGlyProCysSerThrThrCysGlyLeuGlyMetAlaThrArgValSerA
        670                 690                 710
ACCAGAACCGCTTCTGCCGACTGGAGACCCAGCGCCGCCTGTGCCTGTCCAGGCCCTGCC
snGlnAsnArgPheCysArgLeuGluThrGlnArgArgLeuCysLeuSerArgProCysP
        730                 750                 770
CACCCTCCAGGGGTCGCAGTCCACAAAACAGTGCCTTCTAGAGCCGGGCTGGGAATGGGG
roProSerArgGlyArgSerProGlnAsnSerAlaPheEnd
        790                 810                 830
ACACGGTGTCCACCATCCCCAGCTGGTGGCCCTGTGCCTGGGCCCTGGGCTGATGGAAGA
        850                 870                 890
TGGTCCGTGCCCAGGCCCTTGGCTGCAGGCAACACTTTAGCTTGGGTCCACCATGCAGAA
        910                 930                 950
CACCAATATTAACACGCTGCCTGGTCTGTCTGGATCCCGAGGTATGGCAGAGGTGCAAGA
        970                 990                1010
CCTAGTCCCCTTTCCTCTAACTCACTGCCTAGGAGGCTGGCCAAGGTGTCCAGGGTCCTC
       1030                1050                1070
TAGCCCACTCCCTGCCTACACACACAGCCTATATCAAACATGCACACGGGCGAGCTTTCT
       1090                1110                1130
CTCCGACTTCCCCTGGGCAAGAGATGGGACAAGCAGTCCCTTAATATTGAGGCTGCAGCA
       1150                1170                1190
GGTGCTGGGCTGGACTGGCCATTTTTCTGGGGGTAGGATGAAGAGAAGGCACACAGAGAT
       1210                1230                1250
TCTGGATCTCCTGCTGCCTTTTCTGGAGTTTGTAAAATTGTTCCTGAATACAAGCCTATG
       1270
CGTGAAAAAAAAAAAAAAAAAAAAA
```

FIG.1B

```
              1                                                    50
CTGF-1aa   MTAASMGPVR VAFVVLLALC SRPAV.GQNC SGPCRCPDEP APRCPAGVSL
CTGF-3aa   ....MRGTPK THLLAFSLLC LLSKVRTQLC PTPCTCP.WP PPRCPLGVPL

           51                                                     100
CTGF-1aa   VLDGCGCCRV CAKQLGELCT ERDPCDPHKG LFCDFGSPAN RKIGVC.TAK
CTGF-3aa   VLDGCGCCRV CARRLGEPCD QLHVCDASQG LVCQPGAGPG GRGALCLLAE

           101                                                    150
CTGF-1aa   DGAPCIFGGT VYRSGESFQS SCKYQCTCLD GAVGCMPLCS MDVRLPSPDC
CTGF-3aa   DDSSCEVNGR LYREGETFQP HCSIRCRCED GGFTCVPLCS EDVRLPSWDC

           151                                                    200
CTGF-1aa   PFPRRVKLPG KCCEEWVCDE PKDQTVVGPA LAAYRLEDTF GPDPTMIRAN
CTGF-3aa   PHPRRVEVLG KCCPEWVCGQ GGGLGTQPLP AQGPQFSGLV SSLPPGVP..

           201                                                    250
CTGF-1aa   CLVQTTEWSA CSKTCGMGIS TRVTNDNASC RLEKQSRLCM VRPCEADLEE
CTGF-3aa   CPEWSTAWGP CSTTCGLGMA TRVSNQNRFC RLETQRRLCL SRPCPPSRGR

           251                                                    300
CTGF-1aa   NIKKGKKCIR TPKISKPIKF ELSGCTSMKT YRAKFCGVCT DGRCCTPHRT
CTGF-3aa   SPQNSAF... .......... .......... .......... ..........

           301                                                    350
CTGF-1aa   TTLPVEFKCP DGEVMKKNMM FIKTCACHYN CPGDNDIFES LYYRKMYGDM
CTGF-3aa   .......... .......... .......... .......... ..........

           351
CTGF-1aa   A
CTGF-3aa   .
```

FIG.2

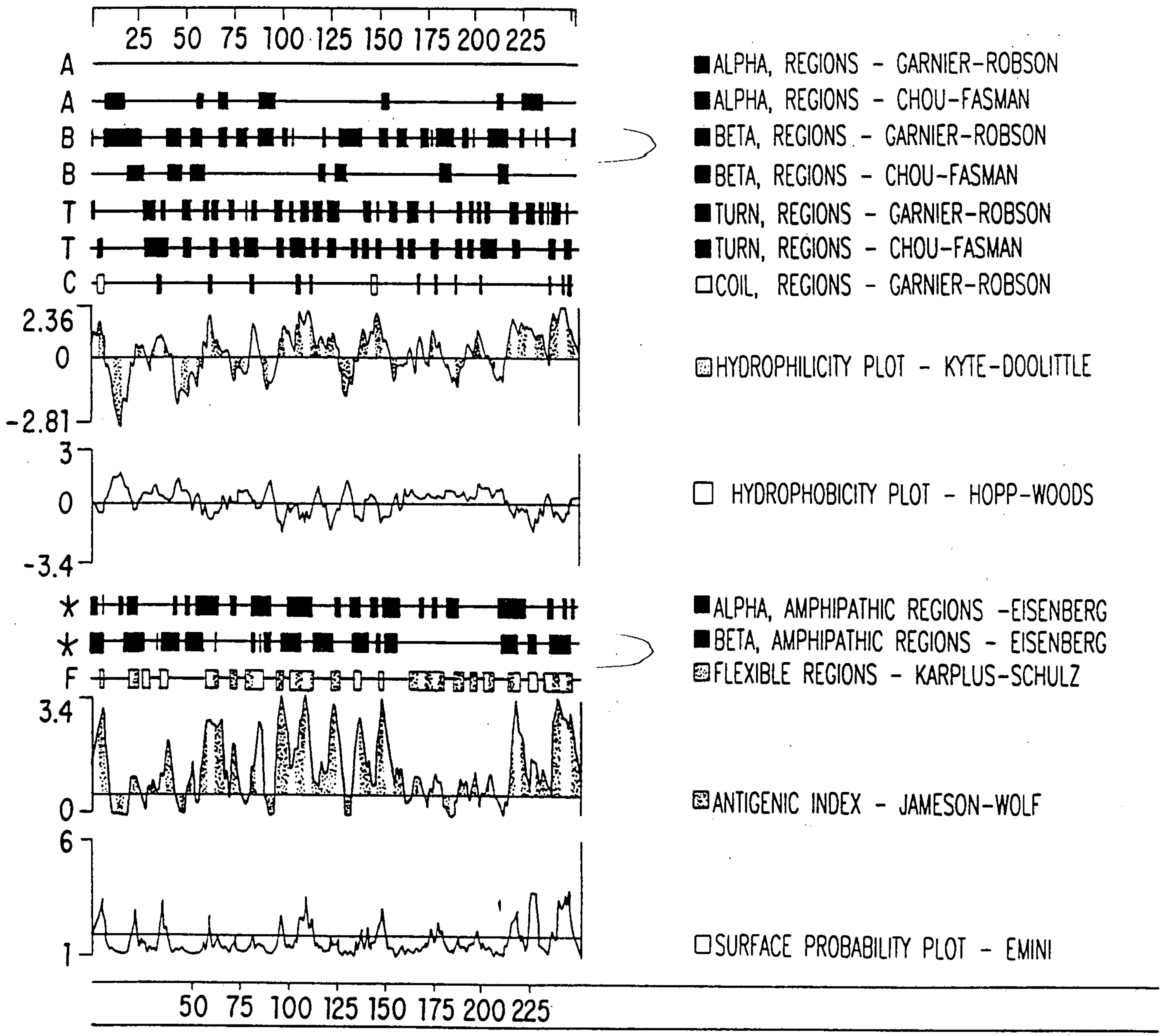
25 50 75 100 125 150 175 200 225
A
A
B
B
T
T
C
2.36
0
-2.81
3
0
-3.4
*
*
F
3.4
0
6
1
50 75 100 125 150 175 200 225
ALPHA, REGIONS - GARNIER-ROBSON
ALPHA, REGIONS - CHOU-FASMAN
BETA, REGIONS - GARNIER-ROBSON
BETA, REGIONS - CHOU-FASMAN
TURN, REGIONS - GARNIER-ROBSON
TURN, REGIONS - CHOU-FASMAN
COIL, REGIONS - GARNIER-ROBSON
HYDROPHILICITY PLOT - KYTE-DOOLITTLE
HYDROPHOBICITY PLOT - HOPP-WOODS
ALPHA, AMPHIPATHIC REGIONS -EISENBERG
BETA, AMPHIPATHIC REGIONS - EISENBERG
FLEXIBLE REGIONS - KARPLUS-SCHULZ
ANTIGENIC INDEX - JAMESON-WOLF
SURFACE PROBABILITY PLOT - EMINI

FIG.3